Schreiber, David

80837

From:

Ramirez, Delia

Sent:

Thursday, November 21, 2002 11:59 AM Schreiber, David

To: Subject:

case 09/854844

Hi David,

I was wondering if you could do an alignment for me. It is seq id 1 against the DNA of accession XM_093852 and seq id 2 against the protein encoded in XM_093852, (LOC166414). Applicant's argue that this entry has 99% similarity to their seq id 2 but I could not find this in the first seach I did.

Thanks,

Delia

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
1911 S. Clark Street, Crystal Mall 1, 10D04, Mail room 10D01
Arlington, VA 22202
(703) 306-0288
delia.ramirez@uspto.gov

U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's Name:		Serial Number:	
Date:	Phone:	Art U	Jnit:
Search Topic: Please write a detailed statement of terms that may have a special mean please attach a copy of the sequent	ning. Give examples or relevent of	citations, authors, keywords,	etc., if known. For sequences,
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Date completed: 1/121 Searcher: 0.5.6.70 Terminal time: 42 Elapsed time: 6 CPU time:	STAFF USE Search Vivie o		Vendors IG STN Dialog APS
Total time: Number of Searches: Number of Databases:		N.A. Sequence A.A. Sequence Structure Bibliographic	Geninfo SDC DARC/Questel Other Compuser Www

21 14:44:33 2002

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//note="Tryp.SPC: Region: Trypsin-like serine protease"
//db_xref="CDD:smart00020"
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242 c 242 q 263 t
                                                           /db_xref="InterimID:166414"
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2; Mismatches
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XM_093852

XM_093852.4 GI:20534015
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NCBI Annotation Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-MAY-2002) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
GENOWE ANNOTATION REFSEQ: This model reference sequence was predicted from NCBI contig NT_022851 by automated computational analysis using gene prediction method: GenomeScan.
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2.055 Million cell updates/sec
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Location/Qualifiers
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          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Maximum Match 100%
Listing first 1 summaries
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Gaps

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Length 987; 2; Indels

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541 TGTGAACAGCTCTACAATCCCATCGGTATCTTCTTGCCAGCACTGGAGCCAGTCATCAAG 601 GAAGACAAGATTTGTGCGTGGTGATACTCAAAACATGAAGGATAGTTGCAAGGGTGATTCT 541 TGTGAACAGCTCTACAATCCCATCGGTATCTTGTTGCCAGCACTGGAGCCAGTCATCAAG

660

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FEATURES

COMMENT

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601 GAAGACAAGATTTGTGCTGGTGATACTCAAAACATGAAGGATAGTTGCAAGGGTGATTCT 660
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Search completed: November 21, 2002, 14:30:56 Job time : 1 secs

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/db_xref-"taxon:9606"

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5.1.3
Compugen Ltd.
 version 5 - 2002 (
GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

November 21, 2002, 14:34:26; Search time 0.001 Seconds (without alignments) 113.488 Million cell updates/sec Run on:

Title: Perfect score:

us-09-854-844-2 1863 1 MGPAGCAFTLLLLGISVCG......GRELTGEPLLTLGDFIYNLK 346

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1 segs, 328 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB 8 Maximum DB 8 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. loc166414.pep:* Database :

SUMMARIES

ACCESSION: XP_09385 Description 328 1 LOC166414 Query Score Match Length DB 93.9 1749 Ş. Result

ALIGNMENTS

similar to epidermis specific serine protease [Homo sapiens]. XP_093852 XP_093852 GI:20534016 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (residues 1 to 328) NCBI Annotation Project. Direct Submission
Submitted (09-MAY-2002) National Center for Biotechnology
Submitted (09-MAY-2002) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
GENOME ANNOTATION REFSEQ: This model reference sequence was predicted from NCBI contig NT_022851 by automated computational analysis using gene prediction method: GenomeScan.
Also see: REFSEQ: accession XM_093852.4 Homo sapiens Homo sapiens RESULT 1 LOC166414 LOCUS DEFINITION ORGANISM AUTHORS TITLE ACCESSION VERSION REFERENCE JOURNAL DBSOURCE KEYWORDS SOURCE COMMENT

May 13, 2002 this sequence version replaced gi:20503620. Location/Qualifiers g

Documentation of NCBI's Annotation Process

FEATURES

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/product="similar to epidermis specific serine protease" 27. .262 SSQVTFTSAILPICLPSVTKQLAIPPFCWVTGWGKVKESSDRDYHSALQEAEVPIIDRQA 180 Gaps 9 1 MGPAGCAFTLLLLLGISVCGQPVYSSRVVGGQDAAAGRWPWQVSLHFDHNFIYGGSLVSE 60 ö Length 328; /region_name="Trypsin-like serine protease" /note="Tryp_SPc" /db_xref="CDD:smart00020" Indels 7 DB 1; /gene="LOC166414" /coded_by="XM_093852.4:1. .987" /db_xref="InterimID:166414" Query Match 93.9%; Score 1749; D Best Local Similarity 99.4%; Pred. No. 0; Matches 326; Conservative 0; Mismatches /region_name="Trypsin" /note="trypsin" /db_xref="CDD:pfam00089" 301 HRVGTVAEAVACIQGWEENAWRFSPRGR 328 /chromosome="4" Query Match Best Local Similarity Protein Region Region 121 CDS q ò ò q οy g ö g ò q òγ g

Search completed: November 21, 2002, 14:34:27 Job time : 1 secs

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